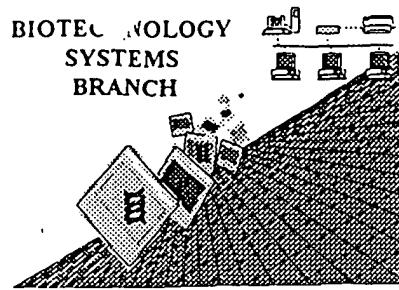


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/785, 738

Source: OIPE

Date Processed by STIC: 6-6-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/785,738

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHIA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

3 <110> APPLICANT: Sauter, Margret M.
4 Lorbiecke, Rene
6 <120> TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
7 CONDITIONS
9 <130> FILE REFERENCE: CropDesign
11 <140> CURRENT APPLICATION NUMBER: US/09/785,738
12 <141> CURRENT FILING DATE: 2001-02-16
14 <160> NUMBER OF SEQ ID NOS: 18
16 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

Does Not Comply
Corrected Diskette Needed

pp. 1-11

ERRORRED SEQUENCES

18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 872
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Rice
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (69)..(668)
 27 <400> SEQUENCE: 1
 28 agacgaacaa aaaacagaat ccatcgccat aatcgaaggt tcgctttgc ttccaccccg 60
 29 caatccac atg gag aac ttc cag gat ggt aag acg gag gtg ata gaa 110
 30 Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu *move to here*
 W--> 31 1 5 10
 W--> 33 gca tgg tac atg gat gat agc gaa gag gac cag agg ctt cct cat cac
 W--> 34 Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His 1
 W--> 35 15 20 25 30
 W--> 37 cgc gaa ccc aaa gaa ttc att cct gtt gat aag ctt aca gaa cta gga
 W--> 38 Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly 1
 W--> 39 35 40 45
 W--> 41 gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac
 W--> 42 Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn 1
 W--> 43 50 55 60
 W--> 45 ctg aag aga atc cgc gaa gcc aga ggt tac tct tat gtg gac att tgt
 W--> 46 Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys 1
 W--> 47 65 70 75
 W--> 49 gat gtg tgc cca gag aag ctg cca aat tat gaa act aac aag atc aag agt
 W--> 50 Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser 1
 W--> 51 80 85 90
 W--> 53 ttc ttt gaa gaa cac ctg cat acc gat gaa gaa ata cgc tat tgt ctt
 W--> 54 Glu Glu His Ieu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu 1
 W--> 55 95 100 105 110
 W--> 57 gaa ggg agt gga tac ttt gat gtg aga gac caa aat gat cag tgg att
 W--> 58 Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile
 W--> 59 115 120 125
 W--> 61 cgt ata gca ctg aag aaa gga ggc atg att gtt ctg cct gca ggg atg

↓
 158 Ala Trp
 ↓
 206 Arg Glu
 ↓
 254 Val Ile
 ↓
 302 Leu Lys
 ↓
 350 Asp Val
 ↓
 398 Phe Phe
 ↓
 446 Glu Gly
 ↓
 494 Arg Ile "hard return" arrows

Formatt
 errors.
 Move
 underlined
 amino acids
 to the end
 of the
 line.
 Then insert
 "hard return"

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

W--> 62 Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met
W--> 63 130 135 140
W--> 65 tac cac cgc ttt acg ttg gac acc gac aac tat atc aag gca atg cga
W--> 66 Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg
W--> 67 145 150 155
W--> 69 ctg ttt gtt ggc gat cct gtt tgg aca ccc tac aac cgt ccc cat gac
W--> 70 Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp
W--> 71 160 165 170
W--> 73 cat ctt cct gca aga aag gag ttt ttg gct aaa ctt ctc aag tca gaa
W--> 74 Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu
W--> 75 175 180 185 190
W--> 77 ggt gaa aat caa gca gtt gaa ggc ttc tga gggttttgtt gggctcctgc
W--> 78 Asn Gln Ala Val Glu Gly Phe
W--> 79 195 200

E--> 81 actgcggttc tatattcaac ctgaataaga tgtgctatacg caatgtaaat ttagcacagt 748
E--> 82 ggctatggtc gccactcacc aacttgaagt gaaagattt atgattttt 808
E--> 83 tgtatcaatc ggcataatgc atttccgaaa tgtgtttca ataaacagga gtcataa 868
E--> 84 tgaa 872

121 <210> SEQ ID NO: 3
122 <211> LENGTH: 980
123 <212> TYPE: DNA
124 <213> ORGANISM: Rice
126 <220> FEATURE:
127 <221> NAME/KEY: CDS
128 <222> LOCATION: (139)..(735)
130 <400> SEQUENCE: 3

131 cggacgcgtg ggcagattgc gttgagctga agctgtcgt gtgactctt tacaccc 60
132 agcttatccg gaatcgggag ggtttccaa taggaaagca actcaggact caggagcggc 120
133 gtctgagagg tttcagag atg gag aac cag ttc cag gat ggc aag gag gag 171
134 Met Glu Asn Gln Phe Gln Asp Gly Lys Glu Glu

W--> 135 1 5 10
W--> 137 gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt
W--> 138 Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
139 15 20 25
W--> 141 cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca
W--> 142 His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
W--> 143 30 35 40
W--> 145 gag tta gga ata tta agc tgg cgc ctg aat gct gat gac tgg gag aat
W--> 146 Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
W--> 147 45 50 55
W--> 149 gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tct tac atg
W--> 150 Asn Leu Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
W--> 151 60 65 70 75
W--> 153 gat att tgt gat gtg tgt cca gaa aag ctg cca aac tat gag gct aag
W--> 154 Cys Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys
W--> 155 80 85 90
W--> 157 ctg aaa aat ttc ttt gaa gaa cac ttg cat act gat gaa gag ata cgc
W--> 158 Asn Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg
W--> 159 95 100 105

Insert
"hard
returns"
where
arrows
indicate

Sam²

219 Val Ile

267 Pro His

315 Glu Leu

363 Asp Glu

411 Asp Ile

459 Leu Lys

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001

TIME: 10:36:54

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

Same²

W--> 161 tat tgt ctt gag gga agt gga tac ttc gat gtc agg gac caa aat gat 507 Tyr Cys
 W--> 162 Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp ↑
 W--> 163 110 115 120
 W--> 165 cag tgg atc cgt gta gca gtg aag aaa ggg ggc atg att gtt ttg cct 555 Gln Trp
 W--> 166 Ile Arg Val Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro ↑
 W--> 167 125 130 135
 W--> 169 gcg gga atg tat cac cgc ttc aca ttg gac agt gac aac tac atc aag 603 Ala Gly
 W--> 170 Met Tyr His Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys ↑
 W--> 171 140 145 150 155
 W--> 173 gca atg cgg ctc ttt gtg gga gag cct gtc tgg acg ccg tac aac cgt 651 Ala Met
 W--> 174 Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg ↑
 W--> 175 160 165 170
 W--> 177 ccc cat gac cat ctg cca gct aga aag gag tat gtc gaa aaa att atc 699 Pro His
 W--> 178 Asp His Leu Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile ↑
 W--> 179 175 180 185
 W--> 181 aac agg ggt gga act caa gct gtc gaa gct cgt taa aggcatatca 745 Asn Arg
 W--> 182 Gly Gly Thr Gln Ala Val Glu Ala Arg ↑
 W--> 183 190 195

E--> 185 agatgtgctt cctagttcgg tggctgttta cactctacag atactgaata aactgtgcta 805
 E--> 186 tcagctgttg caatgggctc ctaccgacat cttacatcat ttggcagtat tttgcacaaa 865
 E--> 187 cccgcttaaa atctccctga aaatacgcac gtcaccatgt cagagtgttt atatacaata 925
 E--> 188 atgacacttc agtccacagt cagcaaggaa ctaatgacaa aaaaaaaaaa aaaaa 980

225 <210> SEQ ID NO: 5

226 <211> LENGTH: 774

227 <212> TYPE: DNA

228 <213> ORGANISM: Tomato

230 <220> FEATURE:

231 <221> NAME/KEY: CDS

232 <222> LOCATION: (1)..(591)

234 <400> SEQUENCE: 5

W--> 235 gca cca gat cca aga gag gat gtc ata cag gca tgg tac atg gat gac
 W--> 236 Pro Arg Glu Asp Val Ile Gln Ala Trp Tyr Met Asp Asp ↑

48 Ala Pro Asp

W--> 237 1 5 10 15

96 Asn Asp Glu

W--> 239 aac gat gag gac cag agg ctt cct cat cac cgt gag cca aag gaa ttt
 W--> 240 Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe ↑

W--> 241 20 25 30

144 Val Ser

W--> 243 gtt tct ctt gac aag ctg gct gaa ctt gga gtt ctc agc tgg aga ctt
 W--> 244 Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu ↑

W--> 245 35 40 45

192 Asp Ala

W--> 247 gat gct gac aat tat gag act gat gag gag ttg aag aaa att cgg gaa
 W--> 248 Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu ↑

W--> 249 50 55 60

240 Asp Arg

W--> 251 gat cgt gga tat tca tac att gat ttc tgt gag gtt tgc cct gag aaa
 W--> 252 Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys ↑

W--> 253 65 70 75 80

288 Leu Pro

W--> 255 cta ccg aat tac gag gag aaa atc aag aac ttt ttt gaa gaa cac ctg
 W--> 256 Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu ↑

W--> 257 85 90 95

336 His Thr

W--> 259 cac acc gac gag gag atc cgt tac gct gtt gca gga agt ggt tac ttt

Same²

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

W--> 260 Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe ↑
W--> 261 100 105 110
W--> 263 gat gtc cgc gat gtg aat gag agc tgg att cgc gtc tgg gta aag aaa
W--> 264 Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys ↑
W--> 265 115 120 125
W--> 267 ggt gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt
W--> 268 Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu ↑
W--> 269 130 135 140
W--> 271 gat tca agc aac tac att aag gca atg cgt ctc ttt gtt ggt gac cca
W--> 272 Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro ↑
W--> 273 145 150 155 160
W--> 275 att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa
W--> 276 Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln ↑
W--> 277 165 170 175
W--> 279 gaa tat gtt gag acg ttt gtc aac gca gat ggc gct ggt cgt gct gtt
W--> 280 Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val ↑
W--> 281 180 185 190
W--> 283 aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt
W--> 284 Ala Ala ↑
W--> 285 195

Sam²
error
SC²
P.
480 Asp Ser
528 Ile Trp
576 Glu Tyr
631 Asn Ala

E--> 287 aataaatatt accatatggg ggctttgctg ttcttgatgt gtgccttact aagcatgttt 691
E--> 288 aatgttgtat tggccacta aataaatcac cccctatggg agattgattt tttatatgca 751
E--> 289 agtggattt attatgtat ttt 774

327 <210> SEQ ID NO: 7

328 <211> LENGTH: 603

329 <212> TYPE: DNA

330 <213> ORGANISM: Tomato

332 <220> FEATURE:

333 <221> NAME/KEY: CDS

334 <222> LOCATION: (3)..(572)

336 <400> SEQUENCE: 7

W--> 337 aa atg gca atc gag tgt aag gca tgg ttt atg gat gaa aat tca gaa 47 Met Ala
W--> 338 Ile Glu Cys Lys Ala Trp Phe Met Asp Glu Asn Ser Glu

W--> 339 1 5 10 15

W--> 341 gat cag cgg cta ccg cac cag aag aac cca ccg gag ttt gtt tca gtg 95 Asp Gln Arg
W--> 342 Leu Pro His Gln Lys Asn Pro Pro Glu Phe Val Ser Val

W--> 343 20 25 30

W--> 345 gag aaa tta gca gta atc gga gtt tta tac tgg aaa ttg aac cct aat 143 Glu Lys
W--> 346 Leu Ala Val Ile Gly Val Leu Tyr Trp Lys Leu Asn Pro Asn

W--> 347 35 40 45

W--> 349 gat tac gag aac gat gaa gaa ttg aaa aaa att cgt caa agt aga ggc 191 Asp Tyr

W--> 350 Glu Asn Asp Glu Glu Leu Lys Ile Arg Gln Ser Arg Gly

W--> 351 50 55 60

W--> 353 tac agc tac atg gac ttg ctg gat ttg tgc cct gag aag gtg gat aac 239 Tyr Ser

W--> 354 Tyr Met Asp Leu Leu Asp Leu Cys Pro Glu Lys Val Asp Asn

W--> 355 65 70 75

W--> 357 tat gag cag aag ttg aaa aat ttc tat acg gag cac ata cac gca gat

W--> 358 Gln Lys Leu Lys Asn Phe Tyr Thr Glu His Ile His Ala Asp

W--> 359 80 85 90 95

Same

Error

SC²
P.
I

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

W--> 361 gag gag ata cgt tac tgt ctg gaa ggg agt gga tat ttt gat gtg aga 335 Glu Glu
W--> 362 Ile Arg Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg
W--> 363 100 105 110
W--> 365 gac aag gat gat cgc tgg att cgc atc tgg atg aag gcc ggt gat atg 383 Asp Lys
W--> 366 Asp Asp Arg Trp Ile Arg Ile Trp Met Lys Ala Gly Asp Met
W--> 367 115 120 125
W--> 369 att gtc ttg cct gct ggg att tac cac cgg ttc acc cta gat act gat 431 Ile Val
W--> 370 Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp
W--> 371 130 135 140
W--> 372 aac tat gtc aag ttg atg agg ttg ttt gtg gga gag ccg gtg tgg acg 479 Asn Tyr
W--> 373 Val Lys Leu Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr
W--> 374 145 150 155
W--> 376 cct tac aat cga cca caa gaa gat cat cca gca agg aag gag tac atc 527 Pro Tyr
W--> 377 Asn Arg Pro Gln Glu Asp His Pro Ala Arg Lys Glu Tyr Ile
W--> 378 160 165 170 175
W--> 380 aag agt gtt act gaa aga gta gga gtg cct ctt aca gca cac taa 572 Lys Ser
W--> 381 Val Thr Glu Arg Val Gly Val Pro Leu Thr Ala His
W--> 382 180 185 190
E--> 384 gacatatttg agctttacaa acctgagagt g 603

420 <210> SEQ ID NO: 9

421 <211> LENGTH: 889

422 <212> TYPE: DNA

423 <213> ORGANISM: Soybean

425 <220> FEATURE:

426 <221> NAME/KEY: CDS

427 <222> LOCATION: (32)..(634)

429 <400> SEQUENCE: 9

430 cgaaccggtc gtagcagaaa aacttgtcac c atg gtt tct tcc gac aag gat 52
431 Met Val Ser Ser Asp Lys Asp

W--> 432 1 5

W--> 434 cca cga gag gat gtc ctt caa gcc tgg tac atg gat gat agt gat gaa 100 Pro Arg

W--> 435 Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
436 10 15 20

W--> 438 gat caa aga ctc ccc cac cac aaa gaa ccc aag gag ttt gtc tcg ttg 148 Asp Gln

W--> 439 Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser Leu

W--> 440 25 30 35

W--> 442 gac caa ctt gct gaa ctt gga gtc ctt agc tgg aaa cta gat gct gat 196 Asp Gln

W--> 443 Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala Asp

W--> 444 40 45 50 55

W--> 446 aac cat gaa aat gat cca gag ctg aag aag att cgt gaa gag cgt ggt 244 Asn His

W--> 447 Glu Asn Asp Pro Glu Leu Lys Ile Arg Glu Glu Arg Gly

W--> 448 60 65 70

W--> 450 tac acc tac atg gat gtt tgt gag gtc tgc cca gaa aag ttg cca aat 292 Tyr Thr

W--> 451 Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro Asn

W--> 452 75 80 85

W--> 454 tat gaa cag aaa atc aaa agc ttc ttt gaa gag cat ctt cac act gat 340 Tyr Glu

W--> 455 Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr Asp

W--> 456 90 95 100

W--> 458 gag gag atc cgc ttt tgt gct gct gga agt ggc tat ttt gat gtt agg 388 Glu Glu

Same
Error
See p. 1

Same
Error
See p. 1

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

W--> 459 Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val Arg
 W--> 460 105 110 115
 W--> 462 gat cgc aat gaa gct tgg att cgt gtg tgg gtc aag aaa gga gga atg 436 Asp Arg
 W--> 463 Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
 W--> 464 120 125 130 135
 W--> 466 atc atc tta cct gcc gga att tat cat cgc ttt acg cta gat gag agc 484 Ile Ile
 W--> 467 Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Ser
 W--> 468 140 145 150
 W--> 470 aac tac att aag gct ttg cgt ttt ttt ggt gag cca gtt tgg act 532 Asn Tyr
 W--> 471 Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp Thr
 W--> 472 155 160 165
 W--> 474 cca tac aat cgt cca aat gac cat ctc cct gca aga caa caa tat gtc 580 Pro Tyr
 W--> 475 Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr Val
 W--> 476 170 175 180
 W--> 478 aag gat ttt gtg gaa aag gat gtt agc agc cat gct gtt gat gcc acc 628 Lys Asp
 W--> 479 Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala Thr
 W--> 480 185 190 195
 W--> 482 gcg taa gatctggttc tgcctaataca tagtaccaca tgaaaaggac caagactttg 684 Ala
 W--> 483 200
 E--> 485 ttgctaaagt aagggttgaa aaaaagaaaa taatgggtgc tttaataaaa gggcctggc 744
 E--> 486 ttgttatgcc ttgatgtacc ctcgccatgt tttttgttgc ctgtccctgt ataaagattg 804
 E--> 487 cattgttata ttattagaat tgggtacaga ataaacataa gcataagtta gcatgctgat 864
 E--> 488 gtatatttat gtaaaaaaaaa ataaa 889

492 <210> SEQ ID NO: 10

493 <211> LENGTH: 200

494 <212> TYPE: PRT

495 <213> ORGANISM: Soybean

497 <400> SEQUENCE: 10

Number of amino acids differ:

- 200 listed

- 210 shown (see next page)

498 Glu Pro Val Val Ala Glu Lys Leu Val Thr Met Val Ser Ser Asp Lys

499 1 5 10 15

500 Asp Pro Arg Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp

501 20 25 30

502 Glu Asp Gln Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser

503 35 40 45

504 Leu Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala

505 50 55 60

506 Asp Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg

507 65 70 75 80

508 Gly Tyr Thr Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro

509 85 90 95

510 Asn Tyr Glu Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr

511 100 105 110

512 Asp Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val

513 115 120 125

514 Arg Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly

515 130 135 140

516 Met Ile Ile Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu

517 145 150 155 160

518 Ser Asn Tyr Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp

Some
Error
See p. 1

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

519 165 170 175
520 Thr Pro Tyr Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr
521 180 185 190
522 Val Lys Asp Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala
523 195 200 205

E--> 524 Thr Ala
525 210 → 200 listed

528 <210> SEQ ID NO: 11

529 <211> LENGTH: 933

530 <212> TYPE: DNA

531 <213> ORGANISM: Cotton

533 <220> FEATURE:

534 <221> NAME/KEY: CDS

535 <222> LOCATION: (33)..(635)

537 <400> SEQUENCE: 11

538 atttttttt aatttgacgg aaaaaaaaaa ct atg acc atg ggt tct gca gac 53
539 Met Thr Met Gly Ser Ala Asp

W--> 540 1 5
W--> 542 aag agg gag gaa gtt att cag gca tgg tac atg gat gat agt gat gaa 101 Lys Arg
W--> 543 Glu Glu Val Ile Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
544 10 15 20
W--> 546 gat cag agg ctt cct cat cac cgt gaa cct aag gaa tat gta tcc ttg 149 Asp Gln
W--> 547 Arg Leu Pro His His Arg Glu Pro Lys Glu Tyr Val Ser Leu
W--> 548 25 30 35
W--> 550 gat aaa ctt gct gag ctt gga gta ctc agc tgg cga ttg gat gct gat 197 Asp Lys
W--> 551 Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu Asp Ala Asp
W--> 552 40 45 50 55
W--> 554 aac tat gaa aat gat gaa gag ttg aag aaa att cgt gaa gaa cga ggt 245 Asn Tyr
W--> 555 Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
W--> 556 60 65 70
W--> 558 tac tcc tac atg gac ttc tgc gag gtt tgc cct gag aag ctt cca aat 293 Tyr Ser
W--> 559 Tyr Met Asp Phe Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
W--> 560 75 80 85
W--> 562 tat gag gag aag ata aaa aat ttc ttc gaa gaa cat att cat act gat 341 Tyr Glu
W--> 563 Glu Lys Ile Lys Asn Phe Phe Glu Glu His Ile His Thr Asp
W--> 564 90 95 100
W--> 566 gag gag atc cgt tac tgt gtg gca gga agt ggt tat ttt gat gta cgg 389 Glu Glu
W--> 567 Ile Arg Tyr Cys Val Ala Gly Ser Gly Tyr Phe Asp Val Arg
W--> 568 105 110 115
W--> 570 gat cat aat gat aaa tgg att cgt gtg tgg gtg aag aaa gga ggc atg 437 Asp His
W--> 571 Asn Asp Lys Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
W--> 572 120 125 130 135
W--> 574 ata gtt tta cct gct gga att tat cat cgc ttt act ctg gat aca gac 485 Ile Val
W--> 575 Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp
W--> 576 140 145 150
W--> 578 aac tat att aag gca atg cgg ctc ttt gtt ggt gat cca att tgg act 533 Asn Tyr
W--> 579 Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro Ile Trp Thr
--> 580 155 160 165
--> 582 ccg tac aat cgt ccg cac gat cat ctt cct gca agg aag gag tat atc 581 Pro Tyr

SGML¹²
Format
Error
refer
to
p.1

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

W--> 583 Asn Arg Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Ile
W--> 584 170 175 180
W--> 586 aag aac ttt ttg cgg gag gaa ggt ggt ggc caa gcc gtt gat gct gcc 629 Lys Asn
W--> 587 Phe Leu Arg Glu Glu Gly Gly Gln Ala Val Asp Ala Ala
W--> 588 185 190 195
W--> 590 gca taa aatcaacatt catctgggtgg tggccaagtc gttgatgctg ccgcataaaa 685 Ala
W--> 591 200
E--> 593 tcagcattca tctctggtat cgtgtcttat aaaatatgaa accccggatt tgggtataata 745
E--> 594 aataagtcta ggcttgcctg cttttgatgc gtggatatgg atcggttatgg ttgttgcctg 805
E--> 595 ctatataattg cctattccat atcgaaaatt cgcaaaacttgc ttagtattt ctacatttt 865
E--> 596 tggcttact accagattgg ctcttaataa tcaaagttt cataatatac attcgtcga 925
E--> 597 cgccggccg 933
633 <210> SEQ ID NO: 13
634 <211> LENGTH: 919
635 <212> TYPE: DNA
636 <213> ORGANISM: Human
638 <220> FEATURE:
639 <221> NAME/KEY: CDS
640 <222> LOCATION: (1)..(564)
642 <400> SEQUENCE: 13
W--> 643 cga aca cgg cac ccg cac tgc gcg tca gtg gtg cag gcc tgg tat atg 48 Arg Thr Arg
W--> 644 His Pro His Cys Ala Ser Val Val Gln Ala Trp Tyr Met
W--> 645 1 5 10 15
W--> 647 gac gac gcc ccg ggc acc cgc ggc aac ccc acc gcc ccg acc ccg gcc 96 Asp Asp Ala
W--> 648 Pro Gly Thr Arg Gly Asn Pro Thr Ala Pro Thr Pro Ala
W--> 649 20 25 30
W--> 651 gcc cag tgc gct gga gca gct gcg cgg ctc ggg gtc ctc tac tgg aag 144 Ala Gln
W--> 652 Cys Ala Gly Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys
W--> 653 35 40 45
W--> 655 ctg gat gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga 192 Leu Asp
W--> 656 Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg
W--> 657 50 55 60
W--> 659 aga gag agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat 240 Arg Glu
W--> 660 Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp
W--> 661 65 70 75 80
W--> 663 aaa cta cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat 288 Lys Leu
W--> 664 Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His
W--> 665 85 90 95
W--> 667 ttg cac ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac 336 Leu His
W--> 668 Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr
W--> 669 100 105 110
W--> 671 ttc gat gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag 384 Phe Asp
W--> 672 Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu
W--> 673 115 120 125
W--> 675 aag gga gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg 432 Lys Gly
W--> 676 Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr
W--> 677 130 135 140
W--> 679 gtc gac gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa 480 Val Asp
W--> 680 Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu

Same
See p. 1

Same
See p. 1

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

W--> 681 145 150 155 160
 W--> 683 ccg gtg tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc 528 Pro Val
 W--> 684 Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg
 W--> 685 165 170 175
 W--> 687 ggg cag tac gtg aaa ttt ctg gca cag acc gcc tag cagtgtgcc 574 Gly Gln
 W--> 688 Tyr Val Lys Phe Leu Ala Gln Thr Ala
 W--> 689 180 185
 E--> 691 tgggaactaa cacgtgcctc gtaaaagggtcc ccaatgtaat gaactgagca gaaaattcaa 634
 E--> 692 tcaactttct ctttgctttt agaggatagc cttgaggttag attatcttc ctttgttaaga 694
 E--> 693 ttattttgatc agaatattttt gtaatgaaag gatctgaaa gcaacttggaa agtgtaaaga 754
 E--> 694 gtcacacccca ttttctgtaa ctcaatcaag actgggtgggt ccatggccct gtgttagttc 814
 E--> 695 attgcatatca ggtttagtcc caaatgaaag tttcatatcc cggaaatgcag ttccttagat 874
 E--> 696 gccccatctgg acgtgaatgc cgcgcctgcg tgtaagaagg tgcaat 920
 732 <210> SEQ ID NO: 15
 733 <211> LENGTH: 972
 734 <212> TYPE: DNA
 735 <213> ORGANISM: Mouse
 737 <220> FEATURE:
 738 <221> NAME/KEY: CDS
 739 <222> LOCATION: (17)..(556)
 741 <400> SEQUENCE: 15
 742 agccggccgccc gcccacc atg gtg cag gcc tgg tat atg gac gag tcc acc gcc 52
 743 Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr Ala
 W--> 744 1 5 10
 W--> 746 gac ccg cgg aag ccc cac cgc gca cag ccc gac cgc ccc gtg agc ctg 100 Asp Pro
 W--> 747 Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser Leu
 748 15 20 25
 W--> 750 gag cag ctg cgc acg ctc gga gtg ctc tat tgg aag cta gat gct gac 148 Glu Gln
 W--> 751 Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp
 752 30 35 40
 W--> 754 aag tat gag aac gat cca gaa cta gaa aag atc cgg aaa atg aga aac 196 Lys Tyr
 W--> 755 Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn
 W--> 756 45 50 55 60
 W--> 758 tac tcc tgg atg gac atc atc acc ata tgc aaa gat aca ctt ccc aat 244 Tyr Ser
 W--> 759 Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn
 W--> 760 65 70 75
 W--> 762 tac gag gag aag atc aag atg ttc ttt gag gaa cat ctg cat ctg gat 292 Tyr Glu
 W--> 763 Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu Asp
 W--> 764 80 85 90
 W--> 766 gag gag atc cgc tac atc ctg gag ggt agt ggg tac ttc gat gtc agg 340 Glu Glu
 W--> 767 Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg
 W--> 768 95 100 105
 W--> 770 gac aag gag gac aag tgg atc cgg att tcc atg gag aag ggg gac atg 388 Asp Lys
 W--> 771 Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp Met
 W--> 772 110 115 120
 W--> 774 att act ctt cct gcc ggc atc tat cac cgc ttc aca ctg gac gag aag 436 Ile Thr
 W--> 775 Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Lys
 W--> 776 125 130 135 140
 W--> 778 aat tac gtg aag gcc atg cgg ctg ttt gtt gga gaa cct gtg tgg aca 484 Asn Tyr

Same
See P.1

Same
See P.1

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

837 <221> NAME/KEY: CDS
 838 <222> LOCATION: (36)..(581)
 840 <400> SEQUENCE: 17
 841 gtactgcgca tggagaccga accggactgt tcaag atg agt gtt ttc gag gca 53
 842 Met Ser Val Phe Glu Ala
 W--> 843 1 5
 W--> 845 tgg tac atg gat gaa gag tcc gga gag gac cag aga ctc ccg cac aaa
 W--> 846 Met Asp Glu Glu Ser Gly Glu Asp Gln Arg Leu Pro His Lys 10 15 20
 W--> 847 149 See #9 on the
 W--> 849 ctg agc ccg aat cag ccc gtc agc gtc cag cag ctg gag cac atc gga 101 Trp Tyr
 W--> 850 Pro Asn Gln Pro Val Ser Val Gln Gln Leu Glu His Ile Gly 149 Leu Ser
 W--> 851 25 30 35 Error
 W--> 852 40 45 50 Summary
 W--> 853 gtc ttt cac tgg aag ctg aac gct gat atc tat gaa aat gac ccc gaa 197 Val Phe
 W--> 854 His Trp Lys Leu Asn Ala Asp Ile Tyr Glu Asn Asp Pro Glu
 W--> 855 55 60 65 Sheet.
 W--> 856 70
 W--> 857 ctg cag aag atc cga gag aag ggt tat tcc ttt atg gac atc ata 245 Leu Gln
 W--> 858 Lys Ile Arg Glu Glu Lys Gly Tyr Ser Phe Met Asp Ile Ile
 W--> 859 75 80 85 Same
 W--> 860 90 95 100 Error
 W--> 861 acc att cac ccg gac aaa ctg ccc gat tac caa aac aaa ctg aaa atg 293 Thr Ile
 W--> 862 His Pro Asp Lys Leu Pro Asp Tyr Gln Asn Lys Leu Lys Met
 W--> 863 105 110 115 See P.
 W--> 864 120 125 130
 W--> 865 ttt tac gaa gag cat ctc cac ctg gac gat gag atc cgt tat att ctg 341 Phe Tyr
 W--> 866 Glu Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu
 W--> 867 135 140 145
 W--> 868 150
 W--> 869 gaa gga tcc tct tat ttt gat gtg cgg gac gaa ggc gac cgc tgg atc 389 Glu Gly
 W--> 870 Ser Ser Tyr Phe Asp Val Arg Asp Glu Gly Asp Arg Trp Ile
 W--> 871 160 165
 W--> 872 170 175 180
 W--> 873 cga ata gcg gtg tct aaa ggc gac ctc atc act tta ccg gcc ggg att 437 Arg Ile
 W--> 874 Ala Val Ser Lys Gly Asp Leu Ile Thr Leu Pro Ala Gly Ile
 W--> 875 185 190 195
 W--> 876 200 205 210
 W--> 877 tac cac aga ttc acc gtg gac gaa agc aac tac act aaa gcc atg cgt 485 Tyr His
 W--> 878 Arg Phe Thr Val Asp Glu Ser Asn Tyr Thr Lys Ala Met Arg
 W--> 879 215 220 225
 W--> 880 230 235 240
 W--> 881 ctg ttc gtg ggt gaa ccc gtc tgg aag gcc tac aac cgt cca gcc gat 533 Leu Phe
 W--> 882 Val Gly Glu Pro Val Trp Lys Ala Tyr Asn Arg Pro Ala Asp
 W--> 883 245 250 255
 W--> 884 260 265 270
 W--> 885 gac ttt gac atc cgc aag gaa tac gtg aac tcg ctg gga agc tcc tga 581 Asp Phe
 W--> 886 Asp Ile Arg Lys Glu Tyr Val Asn Ser Leu Gly Ser Ser
 W--> 887 275 280 285
 W--> 888 290 295 300
 W--> 889 aatgcctgat gggattgatt tagtgctgag aatcagactc tgccgtgcct tanacagaca 641
 W--> 890 nycagcaata gtagagctaa catgtcatta cttagtcata aagacacacc tggatataaag 701
 W--> 891 attat 706

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001

TIME: 10:36:55

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
 L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:31 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:33 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
 L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:35 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:37 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
 L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:41 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
 L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:43 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:45 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
 L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:49 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
 L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:53 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
 L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:57 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
 L:58 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:59 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:61 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
 L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:65 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
 L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:69 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
 L:70 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:73 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
 L:74 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:77 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13
 L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:81 M:254 E: No. of Bases conflict, LENGTH:Input:748 Counted:170 SEQ:1
 L:82 M:254 E: No. of Bases conflict, LENGTH:Input:808 Counted:230 SEQ:1
 L:83 M:254 E: No. of Bases conflict, LENGTH:Input:868 Counted:290 SEQ:1
 L:84 M:254 E: No. of Bases conflict, LENGTH:Input:872 Counted:294 SEQ:1
 L:84 M:252 E: No. of Seq. differs, <211>LENGTH:Input:872 Found:294 SEQ:1
 L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:137 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
 L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:141 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:55

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:145 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:149 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:153 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:157 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:161 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:165 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:169 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:173 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:177 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:181 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:185 M:254 E: No. of Bases conflict, LENGTH:Input:805 Counted:231 SEQ:3
L:186 M:254 E: No. of Bases conflict, LENGTH:Input:865 Counted:291 SEQ:3
L:187 M:254 E: No. of Bases conflict, LENGTH:Input:925 Counted:351 SEQ:3
L:188 M:254 E: No. of Bases conflict, LENGTH:Input:980 Counted:406 SEQ:3
L:188 M:252 E: No. of Seq. differs, <211>LENGTH:Input:980 Found:406 SEQ:3
L:235 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:236 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:239 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:240 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:243 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:247 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:248 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001

TIME: 10:36:55

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

L:251 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:252 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:255 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:257 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:259 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:260 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:263 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:267 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:269 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:271 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:272 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:275 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:279 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:283 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10
L:284 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:287 M:254 E: No. of Bases conflict, LENGTH:Input:691 Counted:60 SEQ:5
L:288 M:254 E: No. of Bases conflict, LENGTH:Input:751 Counted:120 SEQ:5
L:289 M:254 E: No. of Bases conflict, LENGTH:Input:774 Counted:143 SEQ:5
L:289 M:252 E: No. of Seq. differs, <211>LENGTH:Input:774 Found:143 SEQ:5
L:337 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:338 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:341 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:342 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:345 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:346 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:347 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:349 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:350 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:351 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:353 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:354 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:355 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:357 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:359 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7

VERIFICATION SUMMARY DATE: 05/31/2001
PATENT APPLICATION: US/09/785,738 TIME: 10:36:55

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

L:361 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:362 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:365 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:366 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:369 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:372 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:373 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:374 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:376 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:377 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:380 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:381 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:382 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:384 M:254 E: No. of Bases conflict, LENGTH:Input:603 Counted:31 SEQ:7
L:384 M:252 E: No. of Seq. differs, <211>LENGTH:Input:603 Found:31 SEQ:7
L:432 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:434 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:434 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:435 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:438 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:438 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:439 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:440 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:442 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:442 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:443 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:443 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:446 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:446 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:447 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:447 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:448 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:450 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:450 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:451 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:451 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:452 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:454 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:454 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:455 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:455 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001

TIME: 10:36:55

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

L:456 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:458 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:458 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:459 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:459 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:460 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:462 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:462 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:463 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:463 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:466 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:466 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:467 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:467 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:470 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:470 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:471 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:471 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:472 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:474 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:474 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:475 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:475 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:476 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:478 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:478 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:479 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:479 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:482 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:482 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:483 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:485 M:254 E: No. of Bases conflict, LENGTH:Input:744 Counted:112 SEQ:9
L:486 M:254 E: No. of Bases conflict, LENGTH:Input:804 Counted:172 SEQ:9
L:487 M:254 E: No. of Bases conflict, LENGTH:Input:864 Counted:232 SEQ:9
L:488 M:254 E: No. of Bases conflict, LENGTH:Input:889 Counted:257 SEQ:9
L:488 M:252 E: No. of Seq. differs, <211>LENGTH:Input:889 Found:257 SEQ:9
L:525 M:252 E: No. of Seq. differs, <211>LENGTH:Input:200 Found:210 SEQ:10
L:540 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:542 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:542 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:543 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:543 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:546 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:546 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:547 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:547 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001

TIME: 10:36:55

Input Set : A:\es.txt

Output Set: C:\CRF3\05312001\I785738.raw

L:548 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:550 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:550 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:551 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:551 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:552 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:554 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:554 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:555 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:555 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:556 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:558 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:558 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:559 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:559 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:562 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:562 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:563 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:563 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:564 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:566 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:566 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:567 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:567 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:568 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:570 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:570 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:571 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:571 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:572 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:574 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:574 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:575 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:575 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:576 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:578 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:578 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:579 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:579 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:580 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:582 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:582 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:583 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:583 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:584 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:586 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:586 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:587 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:55

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

L:587 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:588 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:590 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:590 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:591 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:593 M:254 E: No. of Bases conflict, LENGTH:Input:745 Counted:113 SEQ:11
L:594 M:254 E: No. of Bases conflict, LENGTH:Input:805 Counted:173 SEQ:11
L:595 M:254 E: No. of Bases conflict, LENGTH:Input:865 Counted:233 SEQ:11
L:596 M:254 E: No. of Bases conflict, LENGTH:Input:925 Counted:293 SEQ:11
L:597 M:254 E: No. of Bases conflict, LENGTH:Input:933 Counted:301 SEQ:11
L:597 M:252 E: No. of Seq. differs, <211>LENGTH:Input:933 Found:301 SEQ:11
L:643 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:644 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:645 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:647 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:648 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:649 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:651 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:652 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:653 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:655 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:656 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:657 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:659 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:660 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:661 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:663 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:664 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:665 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:667 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:668 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:669 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:671 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:672 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:673 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:675 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:676 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:677 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:679 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:680 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:681 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:683 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:684 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:685 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:687 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:688 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:689 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:691 M:254 E: No. of Bases conflict, LENGTH:Input:634 Counted:60 SEQ:13
L:692 M:254 E: No. of Bases conflict, LENGTH:Input:694 Counted:120 SEQ:13

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:55

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

L:693 M:254 E: No. of Bases conflict, LENGTH:Input:754 Counted:180 SEQ:13
L:694 M:254 E: No. of Bases conflict, LENGTH:Input:814 Counted:240 SEQ:13
L:695 M:254 E: No. of Bases conflict, LENGTH:Input:874 Counted:300 SEQ:13
L:696 M:254 E: No. of Bases conflict, LENGTH:Input:920 Counted:346 SEQ:13
L:696 M:252 E: No. of Seq. differs, <211>LENGTH:Input:919 Found:346 SEQ:13
L:744 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:746 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:747 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:750 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:752 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:754 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:755 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:756 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:758 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:759 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:760 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:762 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:763 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:764 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:766 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:767 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:768 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:770 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:771 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:772 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:774 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:775 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:776 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:778 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:779 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:780 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:782 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:783 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:784 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:786 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:12
L:787 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:788 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:790 M:254 E: No. of Bases conflict, LENGTH:Input:646 Counted:112 SEQ:15
L:791 M:254 E: No. of Bases conflict, LENGTH:Input:706 Counted:172 SEQ:15
L:792 M:254 E: No. of Bases conflict, LENGTH:Input:766 Counted:232 SEQ:15
L:793 M:254 E: No. of Bases conflict, LENGTH:Input:826 Counted:292 SEQ:15
L:794 M:254 E: No. of Bases conflict, LENGTH:Input:886 Counted:352 SEQ:15
L:795 M:254 E: No. of Bases conflict, LENGTH:Input:946 Counted:412 SEQ:15
L:796 M:254 E: No. of Bases conflict, LENGTH:Input:972 Counted:438 SEQ:15
L:796 M:252 E: No. of Seq. differs, <211>LENGTH:Input:972 Found:438 SEQ:15
L:828 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:828 M:252 E: No. of Seq. differs, <211>LENGTH:Input:179 Found:184 SEQ:16
L:843 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/785,738

DATE: 05/31/2001
TIME: 10:36:55

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

L:845 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:846 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:849 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:850 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:851 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:853 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:854 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:855 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:857 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:858 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:859 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:861 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:862 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:863 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:865 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:866 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:869 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:870 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:871 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:873 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:874 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:875 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:877 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:878 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:881 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:882 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:883 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:885 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:886 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:887 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:889 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:889 M:254 E: No. of Bases conflict, LENGTH:Input:641 Counted:113 SEQ:17
L:890 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:890 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:890 M:254 E: No. of Bases conflict, LENGTH:Input:701 Counted:173 SEQ:17
L:891 M:254 E: No. of Bases conflict, LENGTH:Input:706 Counted:178 SEQ:17
L:891 M:252 E: No. of Seq. differs, <211>LENGTH:Input:706 Found:178 SEQ:17